

SEQUENCE LISTING

<110> Cihlar, Tomas

<120> NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

<130> 240.1PC

<140> unassigned

<141> 1999-06-10

<150> 60/088,864

<151> 1998-06-11

<150> 60/132,267

<151> 1999-05-03

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 2123

<212> DNA

<213> Unknown

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<223> Description of Unknown Organism: This information
is not available.

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<222> (263)..(1912)

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ggactcagct cccgggaagc aacccagctg cggaggcaac ggcagtgctg ctcctccagc 180

gaaggacagc aggcaggcag acagacagag gtcctggac tggaaaggcct cagccccag 240

ccactggct gggctggcc ca atg gcc ttt aat gac ctc ctg cag cag gtg 292

Met Ala Phe Asn Asp Leu Leu Gln Gln Val

1 5 10

ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc ctc 340

Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu

15

20

25

ccc ctg ctc ctg atg gct tct cac aac acc ctg cag aac ttc act gct	388
Pro Leu Leu Leu Met Ala Ser His Asn Thr Leu Gln Asn Phe Thr Ala	
30 35 40	
gcc atc cct acc cac cac tgc cgc ccg cct gcc gat gcc aac ctc agc	436
Ala Ile Pro Thr His His Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser	
45 50 55	
aag aac ggg ggg ctg gag gtc tgg ctg ccc cgg gac agg cag ggg cag	484
Lys Asn Gly Gly Leu Glu Val Trp Leu Pro Arg Asp Arg Gln Gly Gln	
60 65 70	
cct gag tcc tgc ctc cgc ttc acc tcc ccg cag tgg gga ctg ccc ttt	532
Pro Glu Ser Cys Leu Arg Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe	
75 80 85 90	
ctc aat ggc aca gaa gcc aat ggc aca ggg gcc aca gag ccc tgc acc	580
Leu Asn Gly Thr Glu Ala Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr	
95 100 105	
gat ggc tgg atc tat gac aac agc acc ttc cca tct acc atc gtg act	628
Asp Gly Trp Ile Tyr Asp Asn Ser Thr Phe Pro Ser Thr Ile Val Thr	
110 115 120	
gag tgg gac ctt gtg tgc tct cac agg gcc cta cgc cag ctg gcc cag	676
Glu Trp Asp Leu Val Cys Ser His Arg Ala Leu Arg Gln Leu Ala Gln	
125 130 135	
tcc ttg tac atg gtg ggg gtg ctg ctc gga gcc atg gtg ttc ggc tac	724
Ser Leu Tyr Met Val Gly Val Leu Leu Gly Ala Met Val Phe Gly Tyr	
140 145 150	
ctt gca gac agg cta ggc cgc cgg aag gta ctc atc ttg aac tac ctg	772
Ile Ala Asp Arg Leu Gly Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu	
155 160 165 170	
cag aca gct gtg tca ggg acc tgc gca gcc ttc gca ccc aac ttc ccc	820
Gln Thr Ala Val Ser Gly Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro	
175 180 185	
atc tac tgc gcc ttc cgg ctc tgc ggc atg gct ctg gct ggc atc	868
Ile Tyr Cys Ala Phe Arg Leu Leu Ser Gly Met Ala Leu Ala Gly Ile	
190 195 200	
tcc ctc aac tgc atg aca ctg aat gtg gag tgg atg ccc att cac aca	916
Ser Leu Asn Cys Met Thr Leu Asn Val Glu Trp Met Pro Ile His Thr	
205 210 215	
cgg gcc tgc gtg ggc acc ttg att ggc tat gtc tac agc ctg ggc cag	964
Arg Ala Cys Val Gly Thr Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln	
220 225 230	

ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac ctg Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His Leu 235 240 245 250	1012
cag cta ctg gtc tct gcg cct ttt ttt gcc ttc ttc atc tac tcc tgg Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp 255 260 265	1060
ttc ttc att gag tcg gcc cgc tgg cac tcc tcc ggg agg ctg gac Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Gly Arg Leu Asp 270 275 280	1108
ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag cgg Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg 285 290 295	1156
gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg cag Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln 300 305 310	1204
aag gag ctg acc atg ggc aaa ggc cag gca tcg gcc atg gag ctg ctg Lys Glu Leu Thr Met Gly Lys Gln Ala Ser Ala Met Glu Leu Leu 315 320 325 330	1252
cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg tgg Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu Trp 335 340 345	1300
ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag ggc Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly 350 355 360	1348
ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg gac Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val Asp 365 370 375	1396
ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt cgc Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly Arg 380 385 390	1444
cgg cct gcc cag atg gct gca ctg ctg gca ggc atc tgc atc ctg Arg Pro Ala Gln Met Ala Ala Leu Leu Ala Gly Ile Cys Ile Leu 395 400 405 410	1492
ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct ctt Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser Leu 415 420 425	1540
gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc ttc Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe 430 435 440	1588

ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc atg Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly Met 445 450 455	1636
gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca ctg Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro Leu 460 465 470	1684
gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc tac Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr 475 480 485 490	1732
ggt gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca gag Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu 495 500 505	1780
acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc agg Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg 510 515 520	1828
aaa ggg aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc Lys Gly Lys Gln Thr Arg Gln Gln Glu His Gln Lys Tyr Met Val 525 530 535	1876
cca ctg cag gcc tca gca caa gag aag aat gga ctc tgaggactga Pro Leu Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu 540 545 550	1922
gaagggggct tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca 1982	
caaggaggag gaagagggaaa tggtgaccctt agtgtgggg ttgtggttca ggaaagcattc 2042	
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<213> Unknown	
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Gln Gln Ile Gln Val Thr Leu Val Val Leu Pro Leu Leu Met Ala 20 25 30	
Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His 35 40 45	

Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu
50 55 60

Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg
65 70 75 80

Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala
85 90 95

Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp
100 105 110

Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys
115 120 125

Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly
130 135 140

Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly
145 150 155 160

Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly
165 170 175

Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg
180 185 190

Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr
195 200 205

Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr
210 215 220

Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val
225 230 235 240

Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala
245 250 255

Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala
260 265 270

Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu
275 280 285

Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu
290 295 300

Ser Met Glu Val Leu Arg Ala Ser Leu Gln Lys Glu Leu Thr Met Gly
305 310 315 320

Lys Gly Gln Ala Ser Ala Met Glu Leu Leu Arg Cys Pro Thr Leu Arg
325 330 335

His Leu Phe Leu Cys Leu Ser Met Leu Trp Phe Ala Thr Ser Phe Ala
340 345 350

Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly Phe Gly Val Ser Ile Tyr
355 360 365

Leu Ile Gln Val Ile Phe Gly Ala Val Asp Leu Pro Ala Lys Leu Val
370 375 380

Gly Phe Leu Val Ile Asn Ser Leu Gly Arg Arg Pro Ala Gln Met Ala
385 390 395 400

Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu Leu Asn Gly Val Ile Pro
405 410 415

Gln Asp Gln Ser Ile Val Arg Thr Ser Leu Ala Val Leu Gly Lys Gly
420 425 430

Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe Leu Tyr Thr Gly Glu Leu
435 440 445

Tyr Pro Thr Met Ile Arg Gln Thr Gly Met Gly Ser Thr Met
450 455 460

Ala Arg Val Gly Ser Ile Val Ser Pro Leu Val Ser Met Thr Ala Glu
465 470 475 480

Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr Gly Ala Val Pro Val Ala
485 490 495

Ala Ser Ala Val Thr Val Leu Leu Pro Glu Thr Leu Gly Gln Pro Leu
500 505 510

Pro Asp Thr Val Gln Asp Leu Glu Ser Arg Lys Gly Lys Gln Thr Arg
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<223> Description of Unknown Organism:This information
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<211> 9
<212> DNA
<213> Unknown

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9

<210> 6
<211> 25
<212> DNA
<213> Unknown

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<400> 6
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<210> 9

<211> 29

<212> DNA

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<210> 10

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